Application No. 10/672,937
Amendment and Reply Dated December 29, 2008
In Response to Office Action Dated October 31, 2008

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1.   (Currently Amended)   A method for analyzing sample sequence information relating to at least one sample, the method comprising:

providing a computer;

acquiring sample sequence information relating to the at least one sample, the sample sequence information comprising a plurality of base calls;

assembling consensus sequence information from the sample sequence information;

generating rule-based criteria, the rule-based criteria comprising pre-selected rules for at least one of scan position differences, peak height ratios, peak area ratios, and base composition;

identifying ambiguous bases present within the consensus sequence information by comparing the consensus sequence information to the rule-based criteria, wherein bases that do not meet the pre-selected rules for at least one of the rule-based criteria are labeled ambiguous;; and

outputting the ambiguous bases to a user.

wherein at least one of the assembling, generating, and identifying is performed by the computer.

2.   (Previously Presented) The method of claim 1, wherein the generated rule-based criteria comprises pre-selected rules for scan position differences and the method further comprises

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identifying differences between scan positions of major and minor peaks, within the sample

sequence information, which fall below an empirical threshold.

3.   (Original) The method of claim 2, wherein the empirical threshold associated with

identifying differences between scan positions is in the range of approximately 0 to

approximately 3.

4.   (Previously Presented) The method of claim 1, wherein the generated rule-based criteria

comprises pre-selected rules for scan position differences and the method further comprises

identifying differences between scan positions of major and minor peaks within the sample

sequence information, which reside above, below, or are substantially equivalent to, a user-defined

threshold.

5.   (Previously Presented) The method of claim 1, wherein the generated rule-based criteria

comprises pre-selected rules for peak height ratios and the method further comprises identifying

differences between peak height ratios for major and minor peaks, within the sample sequence

information, which exceed an empirical threshold.

6.   (Previously Presented) The method of claim 5, wherein the empirical threshold associated

with the peak height ratios is in the range of approximately 0.3 to approximately 1.0.

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7.   (Previously Presented) The method of claim 1, wherein the generated rule-based criteria

comprises pre-selected rules for peak area ratios and the method further comprises identifying

differences between peak area ratios of major and minor peaks, within the sample sequence

information, which reside above, below, or are substantially equivalent to, a user-defined threshold.

8.   (Previously Presented) The method of claim 1, wherein the generated rule-based criteria

comprises pre-selected rules for peak area ratios and the method further comprises identifying

differences between peak area ratios for major and minor peaks, within the sample sequence

information, which exceed an empirical threshold.

9.   (Previously Presented) The method of claim 8, wherein the empirical threshold associated

with the peak area ratios is in the range of approximately 0.3 to approximately 1.0.

10.   (Canceled)

11.   (Previously Presented) The method of claim 1, wherein the generated rule-based criteria

comprises pre-selected rules for base composition and the method further comprises determining

major and minor peaks within the sample sequence information and determining if the major and

minor peaks within the sample sequence information are both purines or both pyrimidines.

12-15. (Canceled)

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16.   (Previously Presented) The method of claim 1, further comprising:

excluding identified ambiguous bases from the sample sequence information and

assembling exclusionary consensus sequence information; and

determining variant sequence information between the exclusionary consensus sequence

information and the reference sequence information.

17.   (Canceled)

18.   (Previously Presented) The method of claim 1, wherein the sample sequence information

relating to the at least one sample and the reference sequence information relating to the at least one

reference comprise mitochondrial DNA sequence information.

19-44. (Canceled)

45.   (Previously Presented) The method of claim 1, wherein the identifying ambiguous bases

further comprises assigning a quality value to those bases that have been identified as ambiguous.

46.   (Previously Presented) The method of claim 1, further comprising trimming the consensus

sequence information by trimming the edges of the consensus sequence information.

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47.   (Canceled)